

FIGURE 1A

Map of a First IL-17 Receptor Like cDNA (SEQ ID No: 1)
and Amino Acid (SEQ ID NO: 2)

#5

1 ATAAAAGCGCAGCGTGCGGGTGGCCTGGATCCCGCGCAGTGGCCCCGGCGATGTCGCTCGT 60
M S L V -
61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120
L L S L A A L C R S A V P R E P T V Q C -
121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180
G S E T G P S P E W M L Q H D L I P G D -
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCAAT 240
L R D L R V E P V T T S V A T G D Y S I -
241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAGGCCAC 300
L M N V S W V L R A D A S I R L L K A T -
301 CAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTA 360
K I C V T G K S N F Q S Y S C V R C N Y -
361 CACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACAT 420
T E A F Q T Q T R P S G G K W T F S Y I -
421 CGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGC 480
G F P V E L N T V Y F I G A H N I P N A -
481 AAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA 540
N M N E D G P S M S V N F T S P G C L D -
541 CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACAT 600
H I M K Y K K K C V K A G S L W D P N I -
601 CACTGCTTGTGAAGAAGATGAGGAGACAGTAGAAGTGAACCTTCACAACCACTCCCCTGGG 660
T A C K K N E E T V E V N F T T T P L G -
661 AAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGA 720
N R Y M A L I Q H S T I I G F S Q V F E -
721 GCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGAAGTGGGATACTGA 780
P H Q K K Q T R A S V V I P V T G D S E -
781 AGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACA 840
G A T V Q L T P Y F P T C G S D C I R H -
841 TAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCTTTCCCTCTGGATAACAACAA 900
K G T V V L C P Q T G V P F P L D N N K -
901 AAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTGCTGTCTCTGCTGGTGGCCACATGGGT 960
S K P G G W L P L L L L S L L V A T W V -

Figure 1B

961 GCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTC 1020
L V A G I Y L M W R H E R I K K T S F S -

1021 TACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTT 1080
T T T L L P P I K V L V V Y P S E I C F -

1081 CCATCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCAT 1140
H H T I C Y F T E F L Q N H C R S E V I -

1141 CCTCGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCAC 1200
L E K W Q K K K I A E M G P V Q W L A T -

1201 TCAAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTTCCAATGACGTCAACAGTGTGTG 1260
Q K K A A D K V V F L L S N D V N S V C -

1261 CGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCC 1320
D G T C G K S E G S P S E N S Q D L F P -

1321 CCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGT 1440
L A F N L F C S D L R S Q I H L H K Y V -

1441 GGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCC 1500
V V Y F R E I D T K D D Y N A L S V C P -

1501 CAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCA 1560
K Y H L M K D A T A F C A E L L H V K Q -

1561 GCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCC 1620
Q V S A G K R S Q A C H D G C C S L *

1621 CACCCATGAGAAGCAAGAGACCTTAAAGGCTTCTATCCCACCAATTACAGGGAAAAAAC 1680

1681 GTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAACATTT 1740

1741 TATACCAATAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAAC 1800

1801 TACATTTACAACCTTCAAAGCTGTTTTATACATAGAAAATCAATTACAGCTTTAATTGAAAA 1860

1861 CTGTAACCATTTTGTATAATGCAACAATAAAGCATCTTCAGC 1901

FIGURE 2
Homology of a First IL-17 human Receptor Like Polypeptide
Amino Acid Segeunce (SEQ ID NO: 2) and Known Human IL-17
Receptor Family Member (SEQ ID NO: 3)

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1 .....MSLVLLSLAALCRSAVPREP 20
      || || || |
1 MGAARSPPSAVPGPLLGLLLLLLGV LAPGGASLRLLDHRALVCSQPGLNC 50
21 TVQCGSETGPSPEWMLQHDLPDGLRDLRVEPVTTTSVATGDYSILMNVS 70
      || . . | . . . | : || . : || . . : |
51 TVK..NSTCLDDSWIHPRNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEW 98
71 VLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWT 120
      | . |||| | . : | . | || | . . | : |
99 TLQTDASILYLEGAELSVLQLNTNERLCVRFE....FLSKLRHHHRRWR 143
121 FSYIGFPPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170
      | : | | : . | : | : | . | | | | | | |
144 FTFSHFVVDPDQYEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVT 193
171 KKC VKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QH 213
      | . . ||||| | | . | . | | : | | : |
194 TPCMSSGSLWDPNITVETLEAHQLRVSF TLWNETHYQILLTSFPHMENH 243
214 STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSD 260
      | : | : | . . . | | . . | | : | : | . |
244 SCFEHMHHIPAPRPEEFHQRSNVTLT LRLNKGCCR HQVQIQPFSSCLND 293
261 CIRHKGTVVLCPO.TGVFPPLDNNKSKPGGWLP LLLLLSLLVATWVLVAGI 309
      | : || | | || : | | : . | : : | : | . | : . :
294 CLRHSAT.VSCPEMPDTPEPIPDY MPLWVYWF.ITGISILLVGSVILLIV 341
310 YLMWRHERIKKTSFSTTT.....LLP....PIKVLVVYPSE.ICF 344
      : || : | : | | : | | | : | : | : | :
342 CMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLY 391
345 HHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK....KAAD 390
      : | : || | . || | : : . | . | . | |
392 VDVVLKFAQFLLTACGTEVALDLL EEQATSEAGVMTWVGRQKQEMVESNS 441
391 KVVFLLSNDVNSVCDGTCGKSEGSP.....SENSQDLFPLAFNLFCS 433
      | : : | | . . | : | . | | | | | : |
442 KIIVLC SRGTRAKWQALLGR..GAPVRLRCDHGKPVGD LFTAAMNMILPD 489
481 HVKQQVSAGKRSQACHDGCCSL*..... 503
      . | : : |
540 EMFQPGRMHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECE 589

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FIGURE 3A
Map of a Second Human IL-17 Receptor Like cDNA (SEQ ID NO: 4)
And Amino Acid (SEQ ID NO: 5) Sequences

1 ATAAAGCGC AGCGTGCGGGTG GCCTGGATCCCG CGCAGTGGCCCG GCGATGTCGCTCGT 60
M S L V -
61 GCTGCTAAG CCTGGCCGCGCT GTGCAGGAGCGC CGTACCCCGAGAGCCGACCGTTCAATG 120
L L S L A A L C R S A V P R E P T V Q C -
121 TGGCTCTGA AACTGGGCCATC TCCAGAGTGGAT GCTACAACATGA TCTAATCCCCGGAGA 180
G S E T G P S P E W M L Q H D L I P G D -
181 CTTGAGGGA CCTCCGAGTAGA ACCTGTTACAAC TAGTGTTGCAAC AGGGGACTATTC AAT 240
L R D L R V E P V T T S V A T G D Y S I -
241 TTTGATGAA TGTAAGCTGGGT ACTCCGGGCAGA TGCCAGCATCCG CTGTTGAAGGC CAC 300
L M N V S W V L R A D A S I R L L K A T -
301 CAAGATTTG TGTGACGGGCAA AAGCAACTTCCA GTCCTACAGCTG TGTGAGGCTGGAGTG 360
K I C V T G K S N F Q S Y S C V R L E C -
361 CAGTGGTGC GATCATGGCTCG CTGCGACCTCAA TCTTCTGGGCTC AAGCGATCGTTC TGC 420
S G A I M A R C D L N L L G S S D R S A -
421 TTCAGCCTC CCGAGCGGCTGG GACTGCAGGCGT GGGCCACCAGAC CTGGCTAATTTT TGT 480
S A S R A A G T A G V G H Q T W L I F V -
481 AGTTTTTGT AGAGGGGGGTTT CACCGTGTGCT GGTCTTGAATTC CAGTGCTCAGGC GAT 540
V F V E G G F T V L L V L N S S A Q A I -
541 CTGCCTGCC TCGGCTTCCCAA AGTGCTGGGATT ACAGTGGACATT TTCCTACATCGG CTT 600
C L P R L P K V L G L Q W T F S Y I G F -
601 CCCTGTAGA GCTGAACACAGT CTATTTTATTGG GGCCATAATAT TCCTAATGCAAA TAT 660
P V E L N T V Y F I G A H N I P N A N M -
661 GAATGAAGA TGGCCCTTCCAT GTCTGTGAATTT CACCTCACCAGG CTGCCTAGACCA CAT 720
N E D G P S M S V N F T S P G C L D H I -
721 AATGAAATA TAAAAAAAAGTG TGTCAAGGCCGG AAGCCTGTGGGA TCCGAACATCACT TGC 780
M K Y K K K C V K A G S L W D P N I T A -
781 TTGTAAGAA GAATGAGGAGAC AGTAGAAGTGAA CTTCAACAACCAC TCCCCTGGGAAA CAG 840
C K K N E E T V E V N F T T T P L G N R -
841 ATACATGGC TCTTATCCAACA CAGCACTATCAT CGGGTTTCTCA GGTGTTTGA GCCACA 900
Y M A L I Q H S T I I G F S Q V F E P H -
901 CCAGAAGAA ACAACGCGAGC TTCAGTGGTGAT TCCAGTGACTGG GGATAGTGAAGG TGC 960
Q K K Q T R A S V V I P V T G D S E G A -
961 TACGGTGCA GCTGACTCCATA TTTTCTACTTGT TGGCAGCGACTG CATCCGACATAA AGG 1020
T V Q L T P Y F P T C G S D C I R H K G -

Figure 3B

1021 AACAGTTGT GCTCTGCCCACA AACAGGCGTCCC TTTCCCTCTGGA TAACAACAAAAG CAA 1080
T V V L C P Q T G V P F P L D N N K S K -

1081 GCCGGGAGG CTGGCTGCCTCT CCTCCTGCTGTC TCTGCTGGTGGC CACATGGGTGCT GGT 1140
P G G W L P L L L L S L L V A T W V L V -

1141 GGCAGGGAT CTATCTAATGTG GAGGCACGAAAG GATCAAGAAGAC TTCCTTTTCTAC CAC 1200
A G I Y L M W R H E R I K K T S F S T T -

1201 CACACTACT GCCCCCATTAA GGTTCCTTGTGGT TTACCCATCTGA AATATGTTTCCA TCA 1260
T L L P P I K V L V V Y P S E I C F H H -

1261 CACAATTTG TTA CTTC ACTGA ATTTCTTCAAAA CCATTGCAGAAG TGAGGTCATCCT CGA 1320
T I C Y F T E F L Q N H C R S E V I L E -

1321 AAAGTGGCA GAAAAAGAAAAT AGCAGAGATGGG TCCAGTGCAGTG GCTTGCCACTCA AAA 1380
K W Q K K K I A E M G P V Q W L A T Q K -

1381 GAAGGCAGC AGACAAAGTCGT CTTCTTCTTTT CAATGACGTCAA CAGTGTGTGCGA TGG 1440
K A A D K V V F L L S N D V N S V C D G -

1441 TACCTGTGG CAAGAGCGAGGG CAGTCCCAGTGA GAACTCTCAAGA CCTCTTCCCCCT TGC 1500
T C G K S E G S P S E N S Q D L F P L A -

1501 CTTTAACCT TTTCTG CAGTGA TCTAAGAAGCCA GATTCACTCTGCA CAAATACGTGGT GGT 1560
F N L F C S D L R S Q I H L H K Y V V V -

1561 CTACTTTAG AGAGATTGATAC AAAAGACGATTA CAATGCTCTCAG TGTCTGCCCCAA GTA 1620
Y F R E I D T K D D Y N A L S V C P K Y -

1621 CCACCTCAT GAAGGATGCCAC TGCTTTCTGTGC AGAACTTCTCCA TGTCAAGCAGCAGG T 1680
H L M K D A T A F C A E L L H V K Q Q V -

1681 GTCAGCAGG AAAAAAGATCACA AGCCTGCCACGA TGGCTGCTGCTC CTTGTAGCCCAC CCA 1740
S A G K R S Q A C H D G C C S L *

1741 TGAGAAGCA AGAGACCTTAAA GGCTTCCTATCC CACCAATTACAG GGAAAAAACGTG TGA 1800

1801 TGATCCTGA AGCTTACTATGC AGCCTACAAACA GCCTTAGTAATT AAAACATTTTAT ACC 1860

1861 AATAAAATT TTCAAATATTGC TAACTAATGTAG CATTA ACTAACG ATTGGAACTAC ATT 1920

1921 TACAAC TTC AAAGCTGTTTTA TACATAGAAATC AATTACAGCTTT AATTGAAA ACTG TAA 1980

1981 CCATTTTGA TAATGCAACAAT AAAGCATCTTCAG C 2015

FIGURE 4
Homology of a Second IL-17 Human Receptor Like Polypeptide
Amino Acid Sequence (SEQ ID No: 5) and Known Human IL 17
Receptor Family Mamber (SEQ ID NO: 3)

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1 MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRV 50
1 .....MGAARS 6
51 EPVTTSVATGDYSILMNVSIVLR.ADASIRLL.KATKICVTGKSNFQSYS 98
| ..| :|: . || ||:| | :| |
7 PP..SAVPGPILLGLLLLLLGLVAPGGASLRLLDHRALVCSQPGLNCTVKN 54
99 CVRLECSGAIMARCDLNLGSSDRSA.....SASRAAGTAGVGHQNWLI 142
|: | | | | | | | : | | | | :
55 STCLDDSW.IHPR...NLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL 100
143 ....FVVFVEGGFTVLLVLNSSAQAICL..PRLPKVL..GLQWTFYSYIGF 184
: : : | | . | | | . : : | . | . | | : |
101 QTDASILYLEGAELSVLQLNTN.ERLCVRFEFLSKLRHHHRRWRFTFSHF 149
185 PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKA 234
|: . | : | : | . | | | | | | | |
150 VVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
235 GSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QHSTIIGF 277
| | | | | | | | . | | | | | : | |
200 GSLWDPNITVETLEAHLRVSFLLWNESTHYQILLTSFPHMENHSCFEHM 249
278 SQVFEPHQKKQTRASVVIPTVTDSEGA...TVQLTPYFPTCGSDCIRHKG 324
: | . . . | | . . | | : | : | . | . | | : |
250 HHIPAPRPEEFHQRSNVTTLTLNLKGCCRHHQVQIQPFSSCLNDCLRHS 299
325 TVVLCPQ.TGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH 373
| | | | : | | : . | : : | : | . | . : : | |
300 T.VSCPEMPDTPEPIPDYMLWVYWF.ITGISILLVGSVILLIVCMTWRL 347
374 ERIKTSFSTTT.....LLP....PIKVLVVYPSE.ICFHHTICY 408
: | | | : | | | | : | : : :
348 AGPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLYVDVVLK 397
409 FTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK....KAADKVVFLL 454
| : | | | . | | | : . . | | | . | | . . | : |
398 FAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLC 447
455 SNDVNSVCDGTGCGKSEGSP.....SENSQDLFPLAFNLFCSDLRSQIH 497
| . . | : | . | | | | | : | :
448 SRGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPAC 495
498 LHKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQV 544
| | | | | : | . . | : | | | : | | : | . |
496 FGTYVVVYFSEVSCDGDVPLDGAAPRYPLMDRFEEVYFRIQDLEMFQPG 545
545 SAGKRSQACHDGCCSL*..... 561
: : |
546 RMHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADD 595

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FIGURE 5A
Map of a Third IL-17 Receptor Like cDNA (SEQ ID NO: 6)
and Amino Acid (SEQ ID NO: 7) Sequence

1 ATAAAAGCGCAGCGTGC GGGTGGCCTGGATCCCGCGCAGTGGCCCGGCGATGTCGCTCGT 60
61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120
121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGGAGA 180
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCAAT 240
241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGTGGACATTTTCTACATCGGCTTCC 300
M W T F S Y I G F P -
301 CTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATTAATATTCCTAATGCAAATATGA 360
V E L N T V Y F I G A H N I P N A N M N -
361 ATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAA 420
E D G P S M S V N F T S P G C L D H I M -
421 TGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTT 480
K Y K K K C V K A G S L W D P N I T A C -
481 GTAAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACCACTCCCCTGGGAAACAGAT 540
K K N E E T V E V N F T T T P L G N R Y -
541 ACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACC 600
M A L I Q H S T I I G F S Q V F E P H Q -
601 AGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTA 660
K K Q T R A S V V I P V T G D S E G A T -
661 CGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAA 720
V Q L T P Y F P T C G S D C I R H K G T -
721 CAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTTCCCTCTGGATAACAACAAAAGCAAGC 780
V V L C P Q T G V P F P L D N N K S K P -
781 CGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGG 840
G G W L P L L L L S L L V A T W V L V A -
841 CAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCA 900
G I Y L M W R H E R I K K T S F S T T T -
901 CACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACA 960
L L P P I K V L V V Y P S E I C F H H T -
961 CAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTCGAAA 1020
I C Y F T E F L Q N H C R S E V I L E K -
1021 AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAAGA 1080
W Q K K K I A E M G P V Q W L A T Q K K -
1081 AGGCAGCAGACAAAGTCGTCTTCTCTTTTCCAATGACGTCAACAGTGTGTGCGATGGTA 1140
A A D K V V F L L S N D V N S V C D G T -
1141 CCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCT 1200
C G K S E G S P S E N S Q D L F P L A F -

Figure 5B

1201 TTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCT 1260
N L F C S D L R S Q I H L H K Y V V V Y -
1261 ACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACC 1320
F R E I D T K D D Y N A L S V C P K Y H -
1321 ACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGT 1380
L M K D A T A F C A E L L H V K Q Q V S -
1381 CAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACCCATG 1440
A G K R S Q A C H D G C C S L *
1441 AGAAGCAAGAGACCTTAAAGGCTTCCATCCCACCAATTACAGGGAAAAAACGTGTGATG 1500
1501 ATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAACATTTTATACCAA 1560
1561 TAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACCTAACGATTGGAACTACATTTA 1620
1621 CAACTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAAGTGTAAACC 1680
1681 ATTTTGATAATGCAACAATAAAGCATCTTCAGC 1713

FIGURE 6

Homology of a Third Human IL-17 Receptor Like Polypeptide
Amino Acid Sequence (SEQ ID NO: 7) and Known Human IL-17
Receptor Family Member (SEQ ID NO: 3)

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1 .....MWTFSYIGFP 10
101 QTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFV 150
11 VELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAG 60
151 VDPDQYEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSG 200
61 SLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QHSTIIGFS 103
201 SLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH 250
104 QVFEPHQKKQTRASVVIPTGDSEGA...TVQLTPYFPTCGSDCIRHKG 150
251 HIPAPRPEEFHQRSNVTLTRNLKGCCRHQVQIQPFFSSCLNDCLRHSAT 300
151 VVLCPO.TGVFPFLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRHE 199
301 .VSCPMPDTPPEIPIDYMWVYWF.ITGISILLVGSVILLIVCMTWRLA 348
200 RIKKTSFSTTT.....LLP....PIKVLVVYPSE.ICFHHTICYF 234
349 GPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLYVDVVLKF 398
235 TEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK....KAADKVVFLLS 280
399 AQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCS 448
281 NDVNSVCDGTGCGKSEGSP.....SENSQDLFPLAFNLFCSDLRSQIHL 323
449 RGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACF 496
324 HKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQVS 370
497 GTYVVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQGR 546
371 AGKRSQACHDGCCSL*..... 386
547 MHRVGELSGDNYLRSPGGRQLRAALDRFRDQVRCPDWFECENLYSADDQ 596

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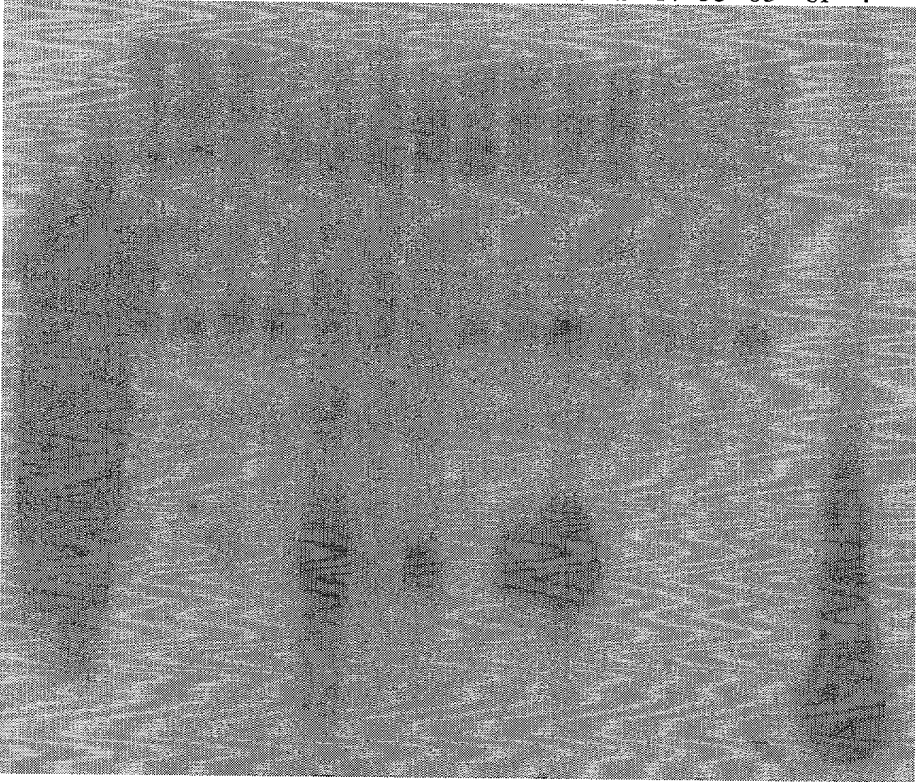
FIGURE 7
Overlap of Amino Acid Sequences of the First (SEQ ID NO: 2),
Second (SEQ ID NO: 5), and Third (SEQ ID NO: 7) Human IL-17
Receptor Like Polypeptides

1	MSLVLLS LAA	LCRS	AVPREP	TVQCGSETG P	SPEWMLQHDL	IPGDLRDLRV
1	MSLVLLS LAA	LCRS	AVPREP	TVQCGSETG P	SPEWMLQHDL	IPGDLRDLRV
51	EPVTTSVATG	DYSILMNV SW	VLRADASIRL	LKATKICVTG	KSNFQSYSCV	
51	EPVTTSVATG	DYSILMNV SW	VLRADASIRL	LKATKICVTG	KSNFQSYSCV	
101	RCNYTEAFQT	QTRPSGGK --	-----	-----	-----	
101	RLECSGAIMA	RCDLNLG SS	DRSASASRAA	GTAGVGHQNW	LIFVVVFVEGG	
119	-----	-----	-----WTF S	YIGFPVELNT	VYFIGAHNIP	
151	FTVLLVLNSS	AQAICLPRLP	KVLGLQWTF S	YIGFPVELNT	VYFIGAHNIP	
1			MWTF S	YIGFPVELNT	VYFIGAHNIP	
143	NANMNEDGPS	MSVNFTSP GC	LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE	
201	NANMNEDGPS	MSVNFTSP GC	LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE	
26	NANMNEDGPS	MSVNFTSP GC	LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE	
193	TVEVNFT TTP	LGNRYMAL IQ	HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD	
251	TVEVNFT TTP	LGNRYMAL IQ	HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD	
76	TVEVNFT TTP	LGNRYMAL IQ	HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD	
243	SEGATVQLTP	YFPTCGSD CI	RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP	
301	SEGATVQLTP	YFPTCGSD CI	RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP	
126	SEGATVQLTP	YFPTCGSD CI	RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP	
293	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
351	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
176	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>	
343	CFHHTICYFT	EFLQNHCR SE	VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV	
401	CFHHTICYFT	EFLQNHCR SE	VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV	
226	CFHHTICYFT	EFLQNHCR SE	VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV	
393	VFLLSND VNS	VCDGTCGK SE	GSPSENSQD L	FPLAFNLFCS	DLRSQIHLHK	
451	VFLLSND VNS	VCDGTCGK SE	GSPSENSQD L	FPLAFNLFCS	DLRSQIHLHK	
276	VFLLSND VNS	VCDGTCGK SE	GSPSENSQD L	FPLAFNLFCS	DLRSQIHLHK	
443	YVVVYFREID	TKDDYNAL SV	CPKYHLMKD A	TAFCAELLHV	KQQVSAGKRS	
501	YVVVYFREID	TKDDYNAL SV	CPKYHLMKD A	TAFCAELLHV	KQQVSAGKRS	
326	YVVVYFREID	TKDDYNAL SV	CPKYHLMKD A	TAFCAELLHV	KQQVSAGKRS	
493	QACHDGC CSL	*				
551	QACHDGC CSL	*				
376	QACHDGC CSL	*				

Figure 8

Northern Blot Expression Analysis of TH00-018
Necropsied Transgenic Founders

	Transgenics								control						
M	1	16	27	29	55	61	20	52	66	2	17	53	65	bl	+



0.54 kb →

Figure 9

Northern Blot Expression Analysis of TH00-018
Hepatectomized Transgenic Founders

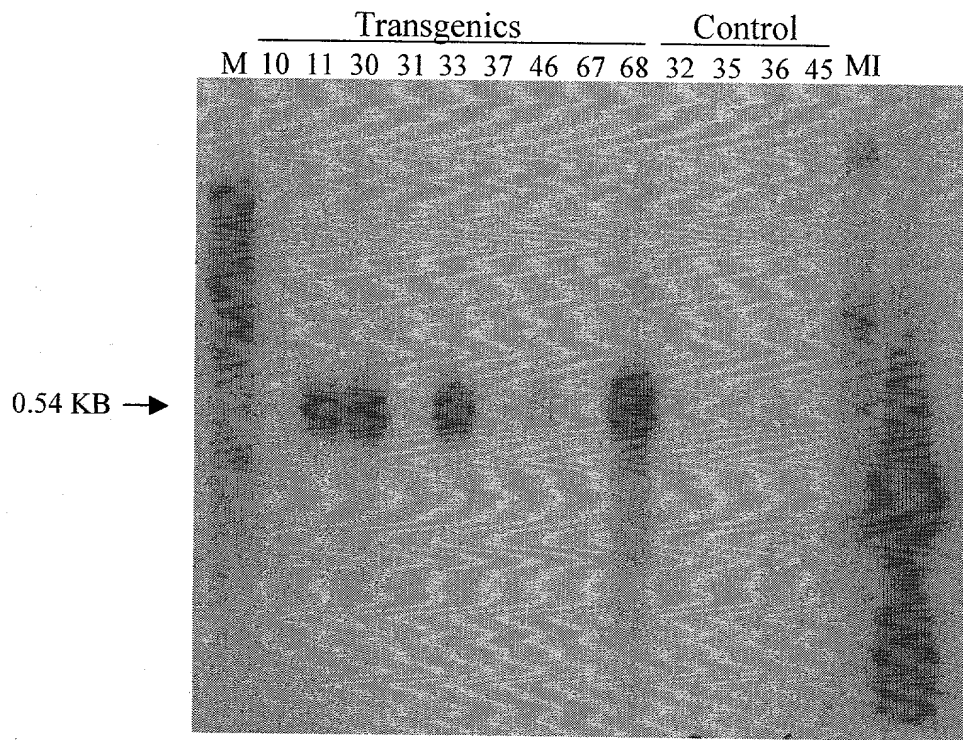


Figure 10

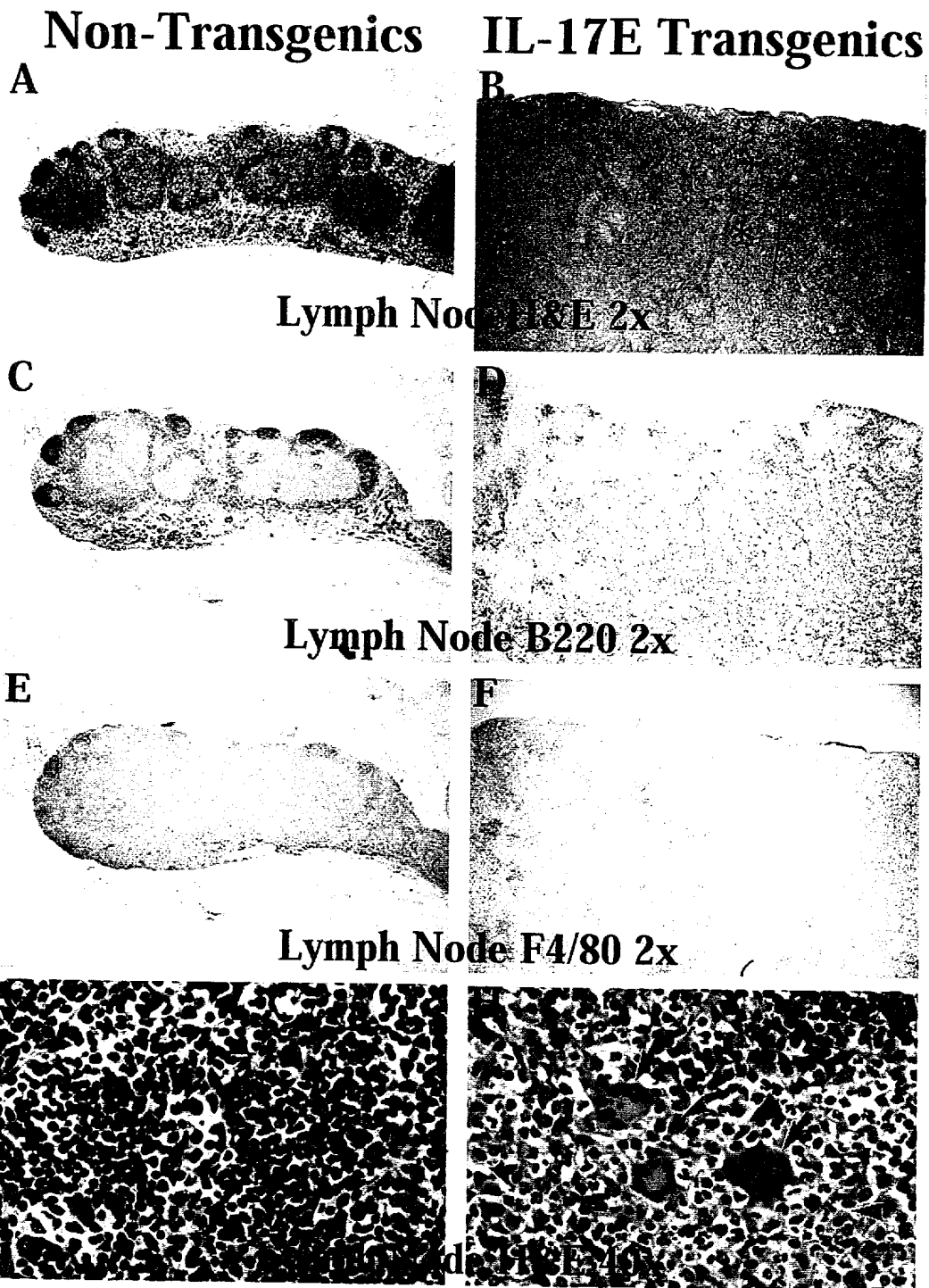


Figure 11

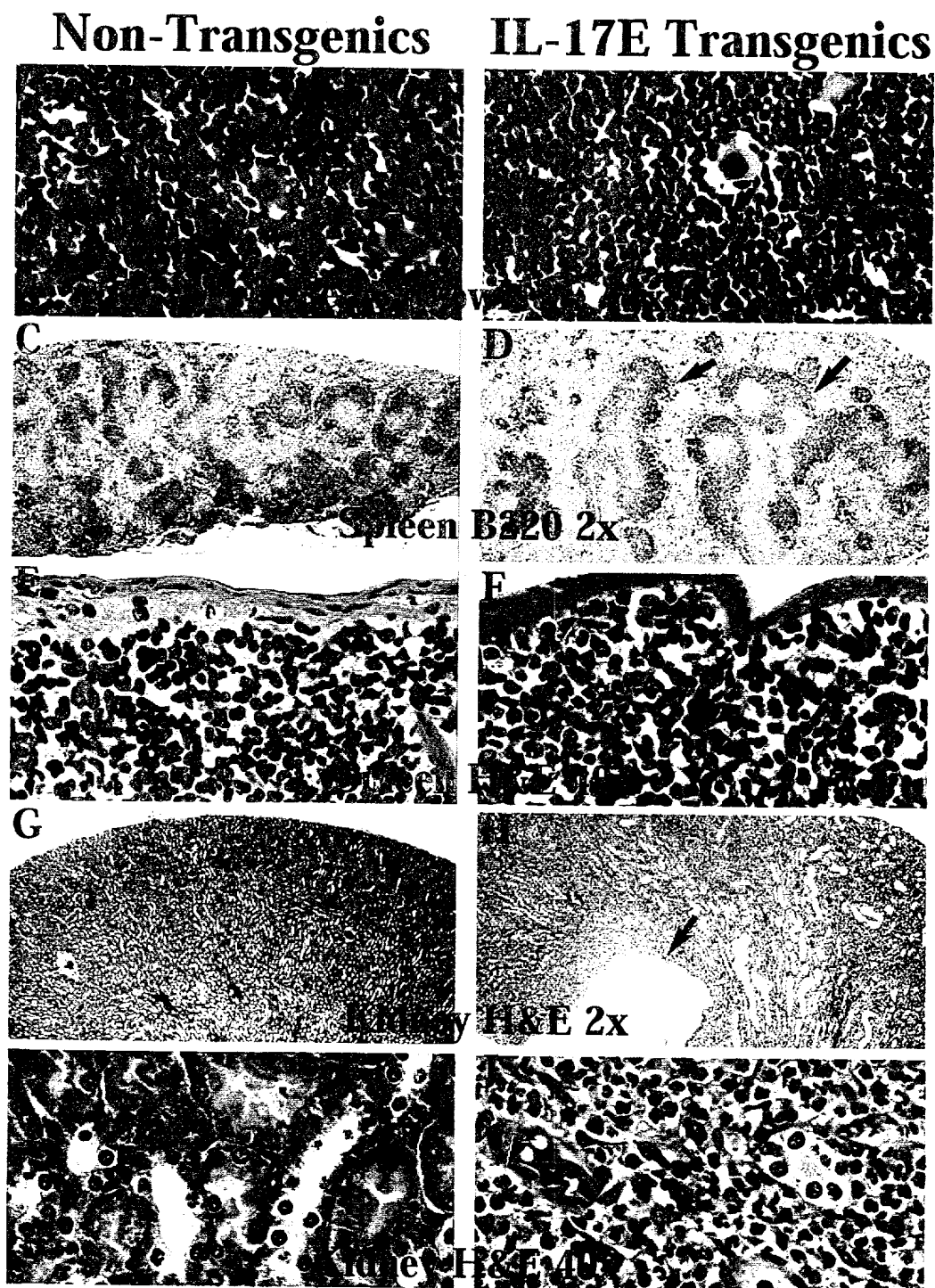


Figure 12

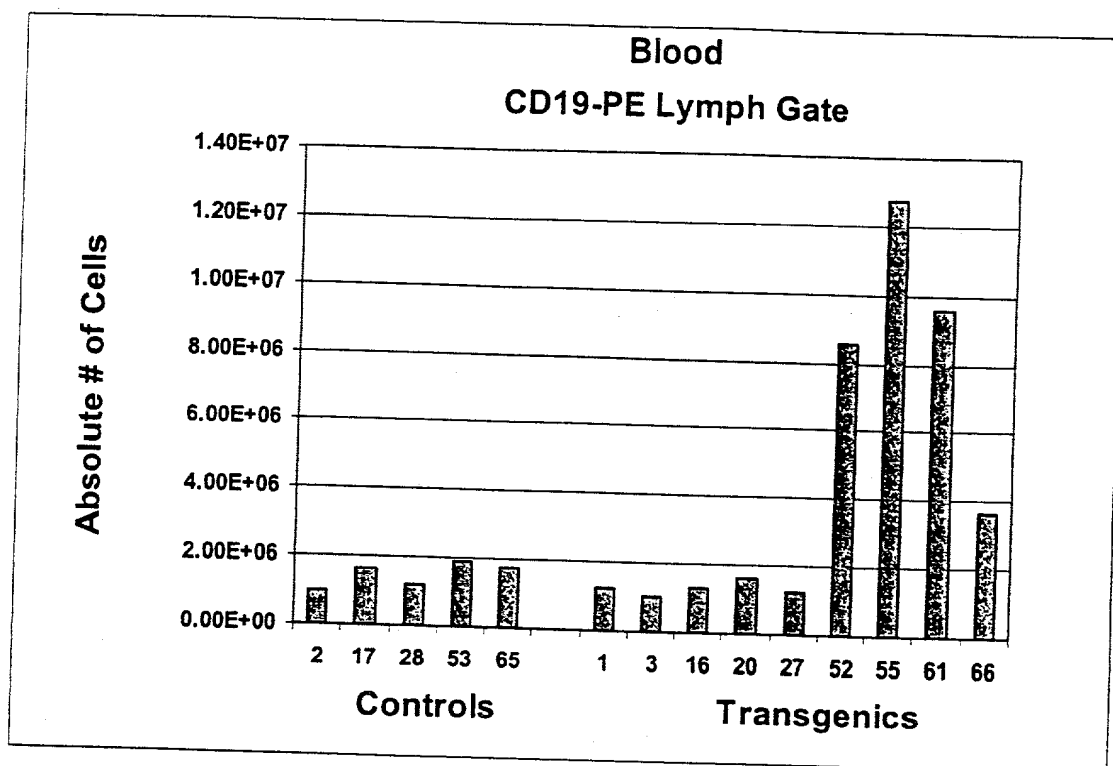


Figure 13

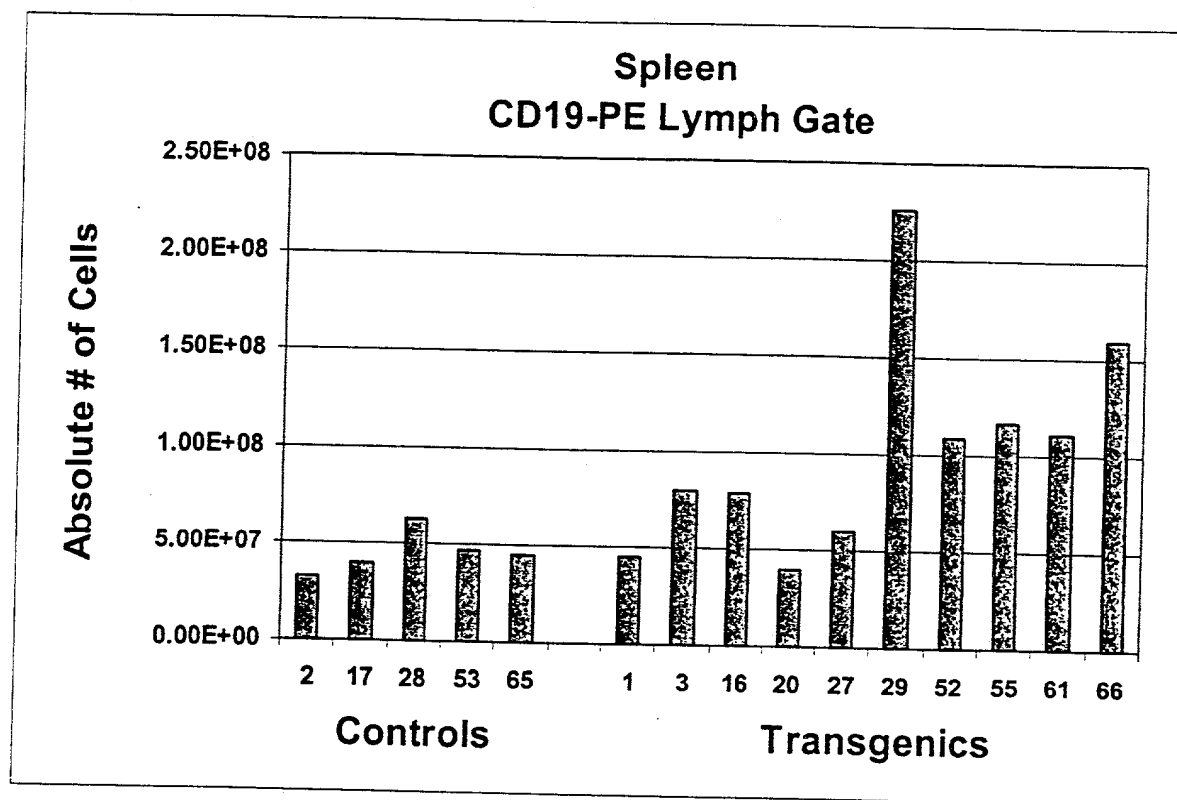


Figure 14

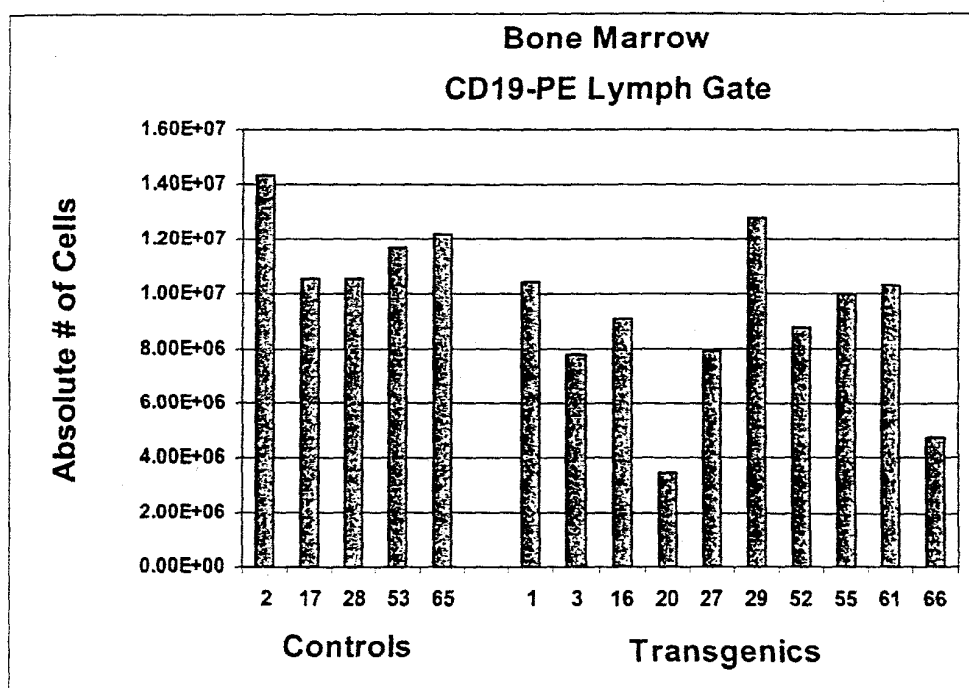


Figure 15

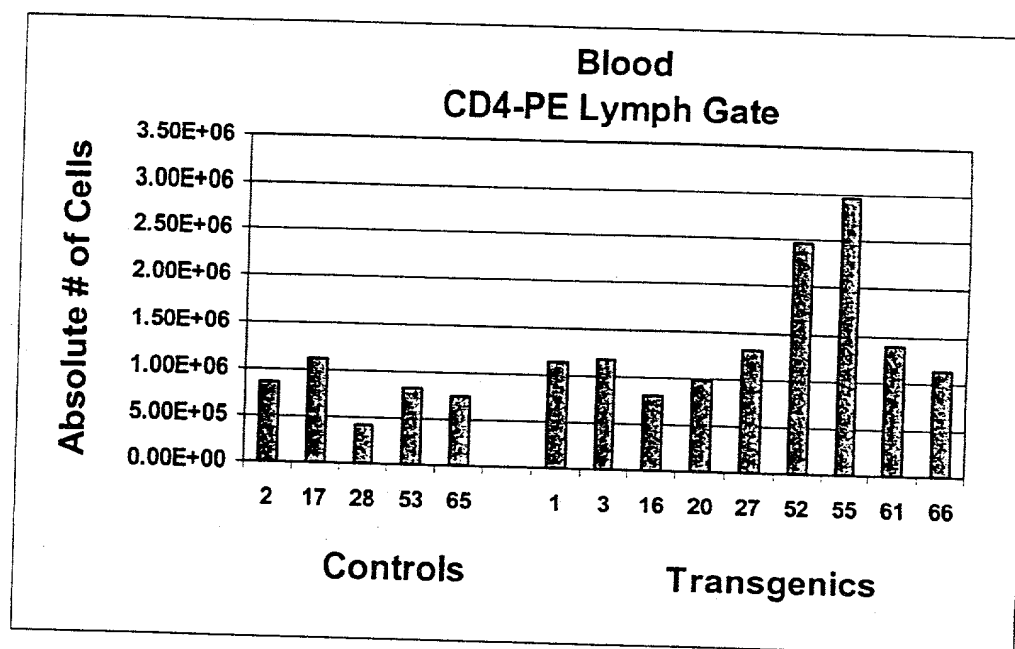


Figure 16

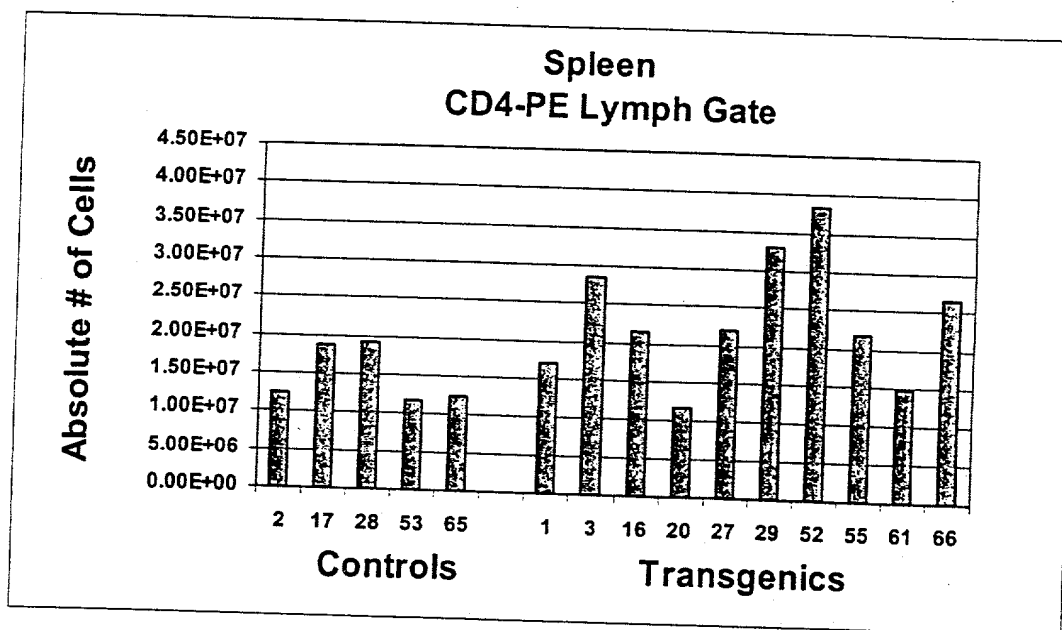
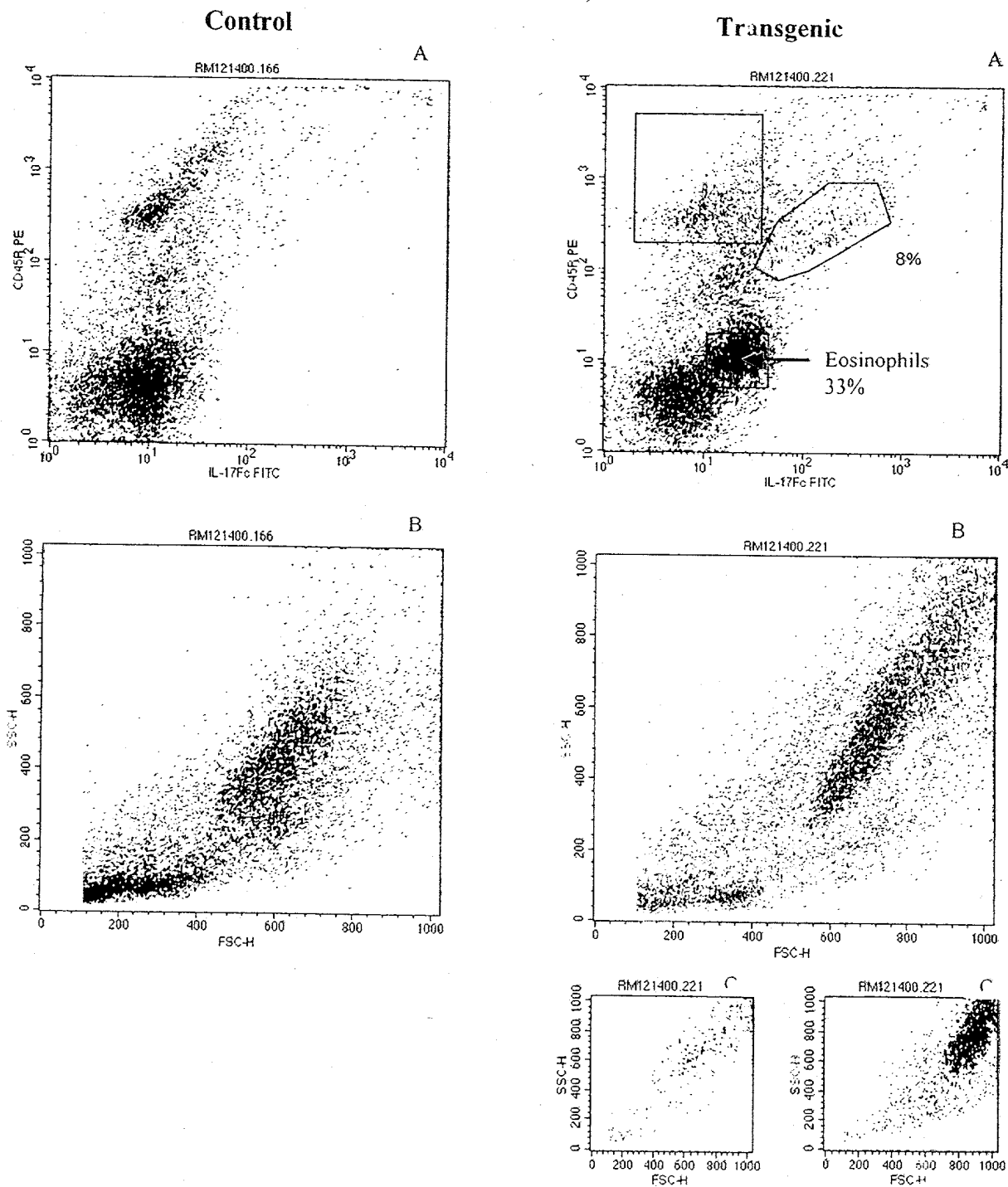


Figure 17

CD45R+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW



Granulocyte-like
cells

Eosinophil-like cells

Figure 18

CD4+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

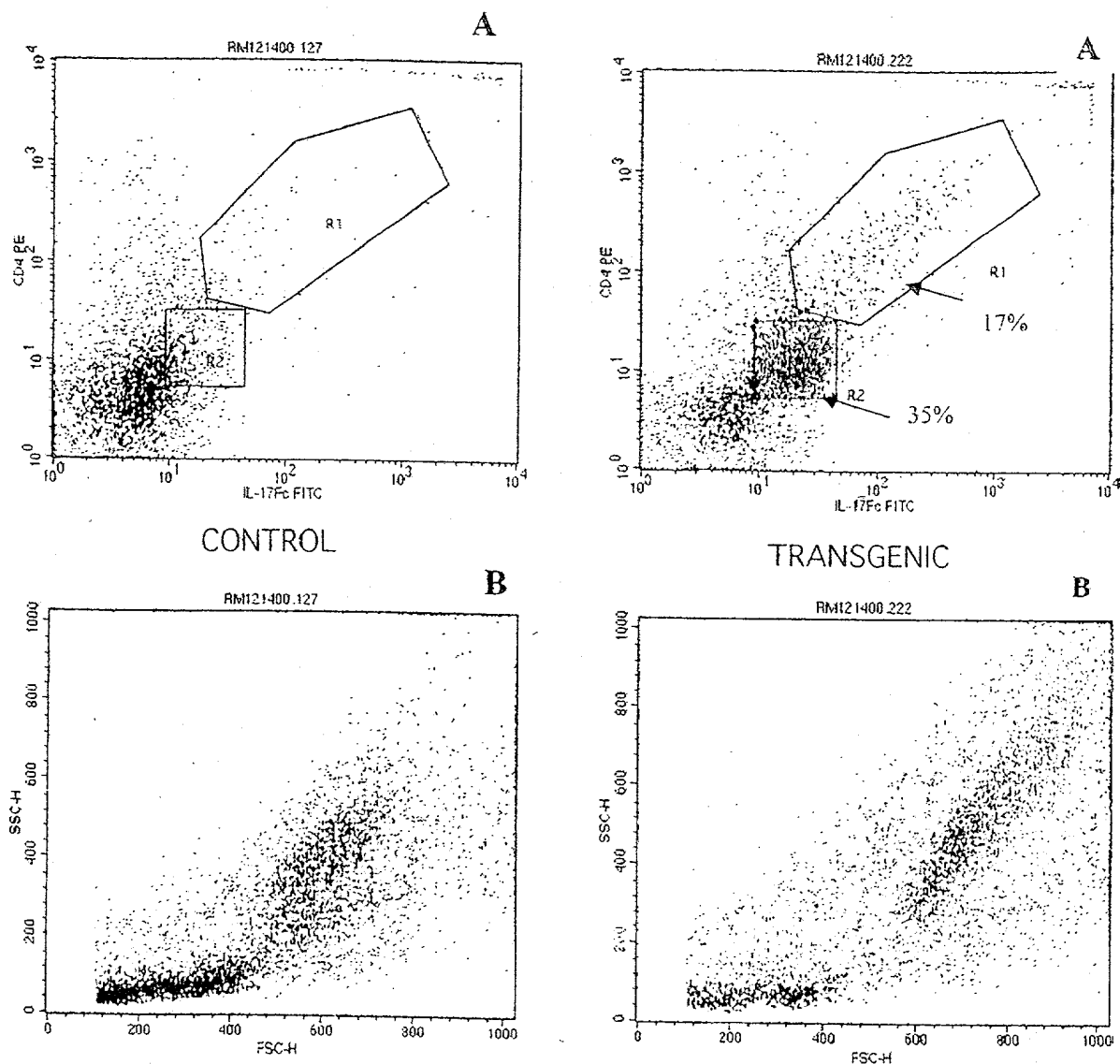


Figure 21

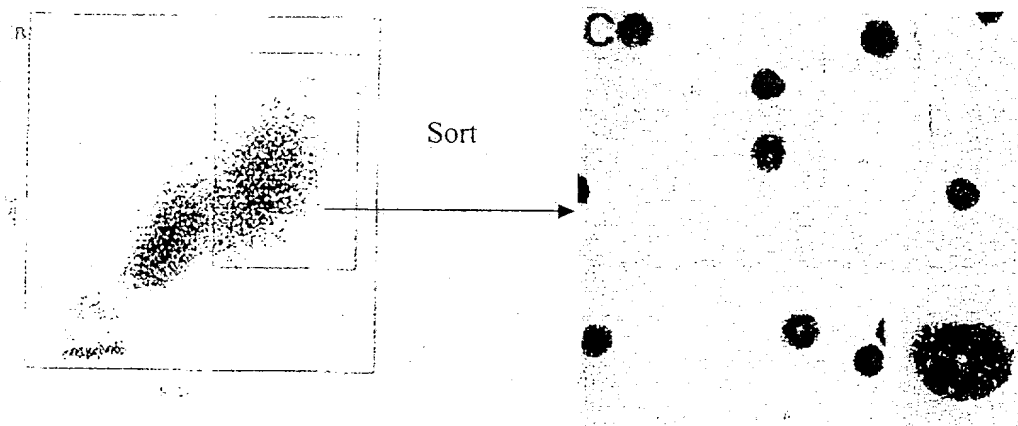


Figure 19

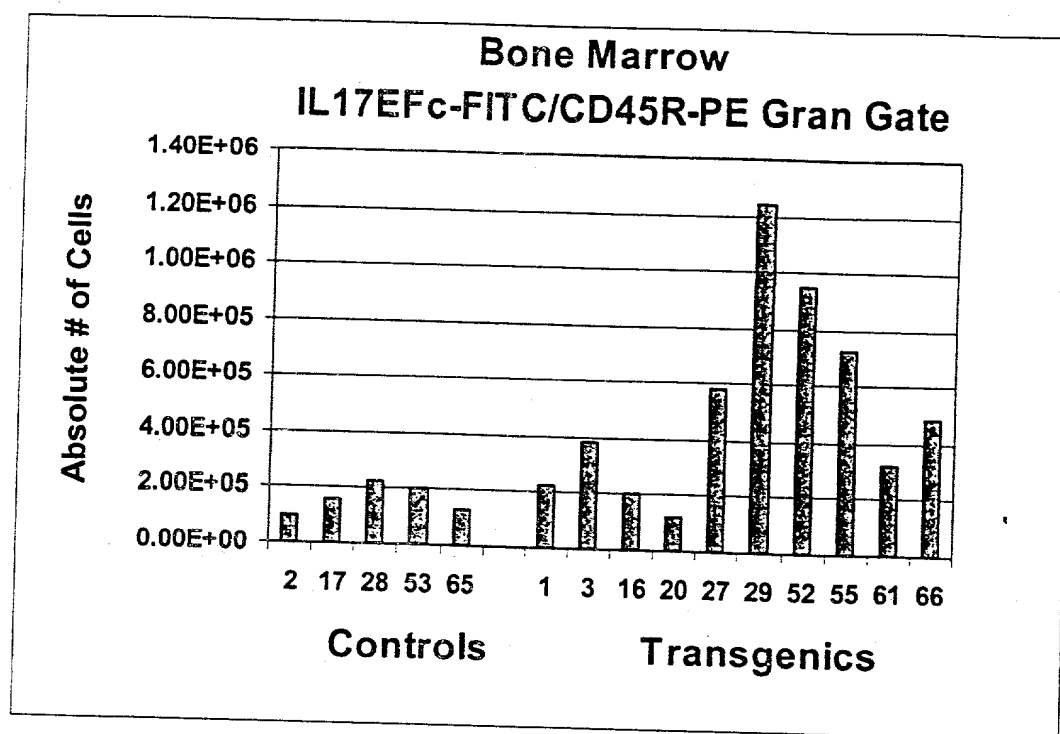


Figure 20

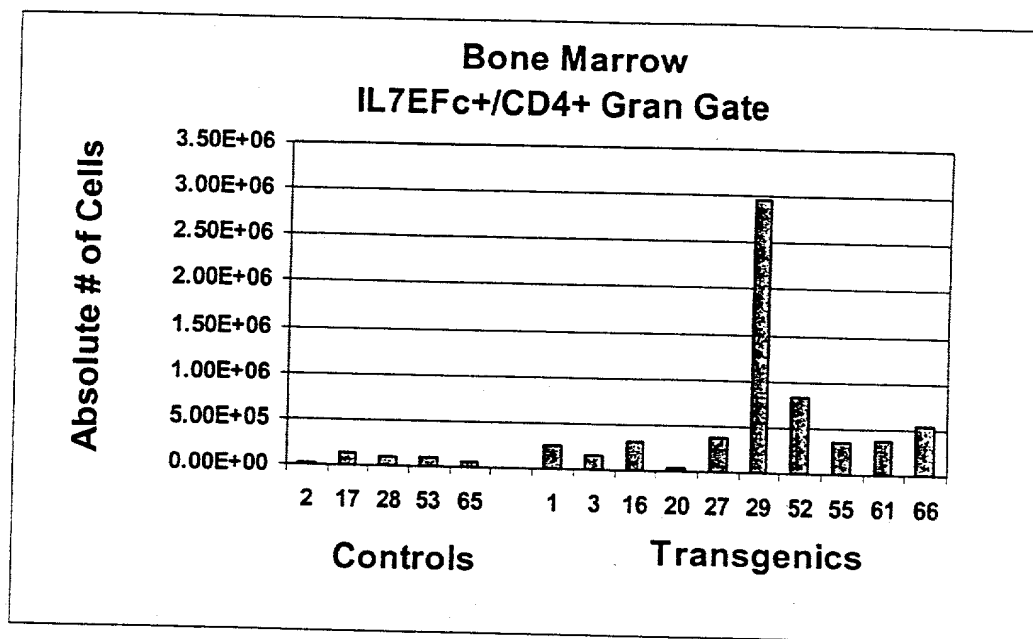


Figure 22

IL-17RB-2 Fusion Protein (SEQ ID NO: 24)

1 **MSLVLLSLAA** **LCRS**AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV
51 EPVTTSVATG DYSILMNVSW VLRADASIRL LKATKICVTG KSNFQSYSCV
101 RCNYTEAFQT QTRPSGGKWT FSYIGFPVEL NTVYFIGAHN IPNANMNEDG
151 PSMSVNFTSP GCLDHIMKYK KKC VKAGSLW DPNITACKKN EETVEVNFTT
201 TPLGNRYMAL IQHSTIIGFS QVFEPHQKKQ TRASVVIPVT GDSEGATVQL
251 TPYFPTCGSD CIRHKGTIVL CPQTGVFPPL DNNKSKPGGW LPAAAEPKSC
301 DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED
351 PEVKFNWYVD GVEVHNATK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK
401 CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLVK
451 GFYPSDIAVE WESNGQPENN YKTTPPVLDG DGSFFLYSKL TVDKSRWQQG
501 NVFSCSVMHE ALHNHYTQKS LSLSPGK*

Figure 23

Fusion Protein for IL-17RB-3 (SEQ ID NO: 25)

1 **MSLVLLSLAA** **LCRS**AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV
51 EPVTTSVATG DYSILMNVS W VLRADASIRL LKATKICVTG KSNFQSYSCV
101 RLECSGAIMA RCDLNLLGSS DRSASASRAA GTAGVGHQTW LIFVVFVEGG
151 FTVLLVLNSS AQAICLPRLP KVLGLQWTFS YIGFPVELNT VYFIGAHNIP
201 NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE
251 TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD
301 SEGATVQLTP YFPTCGSDCI RHKGTVVLCP QTGVFPPLDN NKSKPGGWLP
351 AAAEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM ISRTPEVTCV
401 VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD
451 WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTL PSRDELTKNQ
501 VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV
551 DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK*